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Glancing at host adaptation in Ralstonia solanacearum through comparative genomics of highly host-adapted lineages

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Ralstonia solanacearum is a vascular soil-born plant pathogen with an unusually broad host range. This globally distributed, economically destructive organism has thousands of distinct lineages within a heterogeneous and taxonomically disputed species complex. Some of those lineages can be assigned to ecotypes that include highly host-adapted strains such as the banana Moko disease-causing strains, the cold-tolerant potato brown rot strains (R3bv2) and the recently emerged NPB strains (Not Pathogenic to Banana). The polyphyletic nature of the Moko ecotype and the unexpected closeness of some its lineages to the paraphyletic brown-rot and NPB ecotypes make those highly adapted strains a robust model for study of host adaptation and speciation in general (Cellier, Remenant et al. 2012). Genomes of 10 new strains were produced to complement the 12 publicly available ones. Using a panel of bioinformatics methods, we looked for genetic or evolutionary features that discriminate between ecotypes. There were relatively few divergent features. Those related to known virulence factors were further analyzed for functional clues about host adaptation and ecotype emergence mechanisms. These analyses yield no clear signal, suggesting that the large biological differences between these closely related strains result from differences in gene expression rather than from differences in gene content. Transcriptomic analyses of these strains during host infection are underway to test this hypothesis.

Cellier, G., B. Remenant, et al. (2012). "Phylogeny and population structure of brown rot- and Moko disease-causing strains of Ralstonia solanacearum phylotype II." Applied and Environmental Microbiology **78**(7): 2367-2375.